

1 CGCGTGCAGGTGGCAGTCCTCCCAAAGTACTTGTGTCCGGGTGGT  
 46 GGACTGGATTTCGCTGCCGAGCCCTGGAAGCTGCCTTTCCTTCTCC  
 91 CTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGT  
 MetGlyTrpThrMetArgLeuVa  
 136 CACAGCAGCACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGA  
 lThrAlaAlaLeuLeuLeuGlyLeuMetMetValValThrGlyAs  
 181 CGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGA  
 pGluAspGluAsnSerProCysAlaHisGluAlaLeuLeuAspGl  
 226 GGACACCCTCTTTTGGCAGGGCCTTGAAGTTTCTACCCAGAGTT  
 uAspThrLeuPheCysGlnGlyLeuGluValPheTyrProGluLe  
 271 GGGGAACATTGGCTGCAAGGTTGTTCTTGATTGTAACAACACTACAG  
 uGlyAsnIleGlyCysLysValValProAspCysAsnAsnTyrAr  
 316 ACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGG  
 gGlnLysIleThrSerTrpMetGluProIleValLysPheProGl  
 361 GGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGA  
 yAlaValAspGlyAlaThrTyrIleLeuValMetValAspProAs  
 406 TGCCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTG  
 pAlaProSerArgAlaGluProArgGlnArgPheTrpArgHisTr  
 451 GCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGAT  
 pLeuValThrAspIleLysGlyAlaAspLeuLysGluGlyLysIl  
 496 TCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGC  
 eGlnGlyGlnGluLeuSerAlaTyrGlnAlaProSerProProAl  
 541 ACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGA  
 aHisSerGlyPheHisArgTyrGlnPhePheValTyrLeuGlnGl  
 586 AGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACCTCGAGG  
 uGlyLysValIleSerLeuLeuProLysGluAsnLysThrArgGl  
 631 CTCTTGGAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGA  
 ySerTrpLysMetAspArgPheLeuAsnArgPheHisLeuGlyGl  
 676 ACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTC  
 uProGluAlaSerThrGlnPheMetThrGlnAsnTyrGlnAspSe  
 721 ACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCA  
 rProThrLeuGlnAlaProArgGluArgAlaSerGluProLysHi  
 766 CAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGC  
 sLysAsnGlnAlaGluIleAlaAlaCys  
 811 CATCCGGGCATGTGGCCACACTGCCACCACCGACGATGTGGGTA  
 856 TGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAA  
 901 AAAAAATCATCCAGGAAAAA

Fig. 1

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1 GGAGGTGGGGTGAGACAGGACCAGCCCCCTAAGCCTGGTCAGGCCT  
 46 GATCAAGTGCTGTGGCAGTCATGGTGC GAACGCGGTGGCAGCCTC  
     MetValArgThrArgTrpGlnProH  
 91 ACCCTCCGCCGCCCTGCTTCTCCTGGTGCTCGTGTGGCTCCCC  
     isProProProProLeuLeuLeuLeuValLeuValTrpLeuProG  
 136 AAAGCCTGAGTCTAGACCTGATTGCCTACGTGCCGCAGATAACAG  
     lnSerLeuSerLeuAspLeuIleAlaTyrValProGlnIleThrA  
 181 CCTGGGACCTGGAAGGGAAGATCACAGCCACTACATTCTCTCTGG  
     laTrpAspLeuGluGlyLysIleThrAlaThrThrPheSerLeuG  
 226 AGCAGCCTCGGTGCGTCTTTGATGAGCATGTCTCAACTAAGGACA  
     luGlnProArgCysValPheAspGluHisValSerThrLysAspT  
 271 CCATCTGGCTAGTGGTGGCTTTTCAGCAATGCCTCCAGGGACTTTC  
     hrIleTrpLeuValValAlaPheSerAsnAlaSerArgAspPheG  
 316 AGAACCCACAGACTGCTGCTAAGATCCCGACCTTCCCACAGCTGC  
     lnAsnProGlnThrAlaAlaLysIleProThrPheProGlnLeuL  
 361 TGACTGACGGCCACTATATGACATTACCCCTGTCCCTGGATCAGC  
     euThrAspGlyHisTyrMetThrLeuProLeuSerLeuAspGlnL  
 406 TGCCATGTGAGGACCTGACCGGTGGCAGTGGAGGTGTCCCCGTGC  
     euProCysGluAspLeuThrGlyGlySerGlyGlyValProValL  
 451 TTCGGGTGGGCAATGATTTTGGCTGTTACCAGCGACCCATTTCGA  
     euArgValGlyAsnAspPheGlyCysTyrGlnArgProTyrCysA  
 496 ACGCCCCCTCCCCAGCCAGGGCCCTTACAGTGTGAAGTTCCTTG  
     snAlaProLeuProSerGlnGlyProTyrSerValLysPheLeuV  
 541 TAATGGATGCCGCCGCCGCCACCCAAGGCTGAGACGAAGTGGTCCA  
     alMetAspAlaAlaGlyProProLysAlaGluThrLysTrpSerA  
 586 ACCCCATTTATCTCCACCAAGGAAAGAATCCCAACTCCATTGACA  
     snProIleTyrLeuHisGlnGlyLysAsnProAsnSerIleAspT  
 631 CATGGCCTGGCCGACGGAGCGGCTGTATGATCGTCATAACTTCCA  
     hrTrpProGlyArgArgSerGlyCysMetIleValIleThrSerI  
 676 TCCTCTCTGCCCTGGCCGGCCTCTTGCTCCTGGCTTTCCTGGCAG  
     leLeuSerAlaLeuAlaGlyLeuLeuLeuLeuAlaPheLeuAlaA  
 721 CTTCCACTACGCGT  
     laSerThrThrArg

Fig. 2

10002050-110201

1000611

946 AAAACAGAGAGCAATACCAAGTGGTCATCCAGGCCAAAGACATGG  
 luAsnArgGluGlnTyrGlnValValIleGlnAlaLysAspMetG  
 991 GCGGCCAGATGGGAGGCTTATCGGGGACAACCACTGTGAACATCA  
 lyGlyGlnMetGlyGlyLeuSerGlyThrThrThrValAsnIleT  
 1036 CGCTGACAGATGTCAATGACAACCCACCACGTTTCCCCCAGAACA  
 hrLeuThrAspValAsnAspAsnProProArgPheProGlnAsnT  
 1081 CTATTCATCTTCGAGTTCTTGAATCCTCCCCAGTTGGCACAGCCA  
 hrIleHisLeuArgValLeuGluSerSerProValGlyThrAlaI  
 1126 TTGGAAGTGTCAAAGCAACTGATGCTGACACTGGGAAAAATGCTG  
 leGlySerValLysAlaThrAspAlaAspThrGlyLysAsnAlaG  
 1171 AAGTAGAATACCGAATTATTGATGGTGACGGTACTGATATGTTTG  
 luValGluTyrArgIleIleAspGlyAspGlyThrAspMetPheA  
 1216 ACATCGTGACTGAGAAGGACACACAGGAAGGCATCATCACTGTGA  
 spIleValThrGluLysAspThrGlnGluGlyIleIleThrValI  
 1261 AAAAGCCACTCGACTATGAAAGCCGAAGACTTTATACTCTGAAAG  
 ysLysProLeuAspTyrGluSerArgArgLeuTyrThrLeuLysV  
 1306 TCGAAGCAGAAAACACCCATGTAGATCCCCGTTTTTATTACCTAG  
 alGluAlaGluAsnThrHisValAspProArgPheTyrTyrLeuG  
 1351 GACCATTTAAAGATACTACCATAGTGAAAATCTCTATAGAAGATG  
 lyProPheLysAspThrThrIleValLysIleSerIleGluAspV  
 1396 TGGATGAACCTCCTGTTTTTAGTAGGTCCTCCTATCTGTTTGAAG  
 alAspGluProProValPheSerArgSerSerTyrLeuPheGluV  
 1441 TTCATGAAGATATTGAAGTGGGCACAATCATTGGTACTGTAATGG  
 alHisGluAspIleGluValGlyThrIleIleGlyThrValMetA  
 1486 CAAGGGACCCAGATTCTATTTCCAGCCCCATTAGATTTTCCTTGG  
 laArgAspProAspSerIleSerSerProIleArgPheSerLeuA  
 1531 ATCGCCATACTGACCTTGACAGAATCTTTAACATTCAATTCAGGAA  
 spArgHisThrAspLeuAspArgIlePheAsnIleHisSerGlyA  
 1576 ATGGATCTCTTTATACATCAAAACCTCTTGACCGTGAACCTATCTC  
 snGlySerLeuTyrThrSerLysProLeuAspArgGluLeuSerG  
 1621 AGTGGCATAATTCGTTAGTTATTGCTGCTGAAATCAACAATCCCA  
 lnTrpHisAsnSerLeuValIleAlaAlaGluIleAsnAsnProL  
 1666 AAGAGACAACACGCGTGGCTGTTTTTGTGAGAATTTTGGATGTTA  
 ysGluThrThrArgValAlaValPheValArgIleLeuAspValA  
 1711 ATGACAATGCCCCACAGTTTGCTGTGTTCTATGACACTTTTGTAT  
 snAspAsnAlaProGlnPheAlaValPheTyrAspThrPheValC  
 1756 GTGAAAATGCCAGACCAGGGCAGCTAATACAGACTATAAGTGCAG  
 ysGluAsnAlaArgProGlyGlnLeuIleGlnThrIleSerAlaV

Fig. 3 Continued

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1801 TAGACAAAGATGACCCTTTAGGTGGACAGAAATTTTTTTTCAGTT  
 alAspLysAspAspProLeuGlyGlyGlnLysPhePhePheSerL  
 1846 TAGCTGCTGTCAATCCAACTTCACAGTACAGGATAATGAAGATA  
 euAlaAlaValAsnProAsnPheThrValGlnAspAsnGluAspA  
 1891 ATACTGCCAGAATCTTAACCAGAAAAAATGGATTCAATAGACATG  
 snThrAlaArgIleLeuThrArgLysAsnGlyPheAsnArgHisG  
 1936 AAATCAGTACCTATCTCTTGCCTGTGGTGATATCAGACAATGATT  
 luIleSerThrTyrLeuLeuProValValIleSerAspAsnAspT  
 1981 ACCCGATTTCAGAGCAGCACAGGCACACTGACCATTTCAGTGTGTG  
 yrProIleGlnSerSerThrGlyThrLeuThrIleArgValCysA  
 2026 CTTGTGACAGCCAAGGCAACATGCAATCCTGCAGTGTCTGAAGCCC  
 laCysAspSerGlnGlyAsnMetGlnSerCysSerAlaGluAlaL  
 2071 TGCTCCTCCCTGCCGGCCTCAGCACTGGGGCCTTGATCGCCATCC  
 euLeuLeuProAlaGlyLeuSerThrGlyAlaLeuIleAlaIleL  
 2116 TCCTCTGCATCATCTACTGTTTATAGTAGTACTGTTTGCAG  
 euLeuCysIleIleIleLeuLeuValIleValValLeuPheAlaA  
 2161 CTCTGAAAGGACAGCGAAAAAAGAGCCTCTGATCTTGTCAAAAG  
 laLeuLysGlyGlnArgLysLysGluProLeuIleLeuSerLysG  
 2206 AAGATATCAGAGACAACATTGTGAGCTATAACGATGAGGGTGGTG  
 luAspIleArgAspAsnIleValSerTyrAsnAspGluGlyGlyG  
 2251 GAGAGGAGGACACCCAGGCCTTTGATATCGGCACCCTGAGGAATC  
 lyGluGluAspThrGlnAlaPheAspIleGlyThrLeuArgAsnP  
 2296 CTGCAGCCATTGAGGAAAAAAGCTCCGGCGAGATATTATTCCAG  
 roAlaAlaIleGluGluLysLysLeuArgArgAspIleIleProG  
 2341 AAACGTTATTTATTCTCGGAGGACTCCTACAGCTCCAGATAACA  
 luThrLeuPheIleProArgArgThrProThrAlaProAspAsnT  
 2386 CGGACGTCCGGGATTTTCATTAATGAAAGGCTAAAAGAGCATGATC  
 hrAspValArgAspPheIleAsnGluArgLeuLysGluHisAspL  
 2431 TTGACCCACCGCACCCCCCTACGACTCACTTGCAACCTATGCCT  
 euAspProThrAlaProProTyrAspSerLeuAlaThrTyrAlaT  
 2476 ATGAAGGAAATGATTCCATTGCTGAATCTCTGAGTTCATTAGAAT  
 yrGluGlyAsnAspSerIleAlaGluSerLeuSerSerLeuGluS  
 2521 CAGGTACTACTGAAGGAGACCAAACTACGATTACCTCCGAGAAT  
 erGlyThrThrGluGlyAspGlnAsnTyrAspTyrLeuArgGluT  
 2566 GGGGCCCTCGGTTTAATAAGCTAGCAGAAATGTATGGTGGTGGGG  
 rpGlyProArgPheAsnLysLeuAlaGluMetTyrGlyGlyGlyG  
 2611 AAAGTGACAAAGACTCTTAACGTAGGATATATGTTCTGTTCAAAC  
 luSerAspLysAspS r  
 2656 AAGAGAAAGTAACTCTACCCATGCTGTCTCCACTTCACAATATTT  
 2701 GATATTCAGGAGCATTTCTGTCAGTCAGCACAAATTTTTTCTCA

Fig. 3 Continued

1 AAGATGGTAGCAAAGTAATGAGTTGAGAGTTGCTTTCAGTGGTGT  
 46 GTTACCGGAGATAGAAAAATGAAGGATACAGGCTAAGGGACCAA  
 91 CTGCAGTGTGATGGAACTGAGTTTAAATGATGCCTCTTAGGAAA  
 136 TGAATTCCAACATGTAGTACACTATTCATCTTCGAGTTCCTTGAAT  
 181 CCTCCCCAGTTGGCACAGCCATTGGAAGTGTCAAAGCAACTGATG  
 226 CTGACACTGGGAAAAATGCTGAAGTAGAATACCGAATTATTGATG  
  
 271 GTGACGGTACTGATATGTTTGACATCGTGACTGAGAAGGACACAC  
       MetPheAspIleValThrGluLysAspThrG  
  
 316 AGGAAGGCATCATCACTGTGAAAAGCCACTCGACTATGAGAGCC  
       InGluGlyIleIleThrValLysLysProLeuAspTyrGluSerA  
  
 361 GAAGACTTTTATACTCTGAAAGTCGAAGCAGAAAACACCCATGTAG  
       rgArgLeuTyrThrLeuLysValGluAlaGluAsnThrHisvala  
  
 406 ATCCCCGTTTTTTATTACCTAGGACCATTAAAGATACTACCATAG  
       spProArgPheTyrTyrLeuGlyProPheLysAspThrThrIleV  
  
 451 TGAAAATCTCTATAGAAGATGTGGATGAACCTCCTGTTTTTAGTA  
       alLysIleSerIleGluAspValAspGluProProValPheSerA  
  
 496 GGTCTCCTATCTGTTTGAAGTTCATGAAGATATTGAAGTGGGCA  
       rgSerSerTyrLeuPheGluValHisGluAspIleGluValGlyT  
  
 541 CAATCATTGGTACTGTAATGGCAAGGGACCCAGATTCTATTTCCA  
       hrIleIleGlyThrValMetAlaArgAspProAspSerIleSerS  
  
 586 GCCCCATTAGATTTTCTTGGATCGCCATACTGACCTTGACAGAA  
       erProIleArgPheSerLeuAspArgHisThrAspLeuAspArgI  
  
 631 TCTTTAACATTTCATTTCAGGAAATGGATCTCTTTATACATCAAAC  
       lePheAsnIleHisSerGlyAsnGlySerLeuTyrThrSerLysP  
  
 676 CTCTTGACCGTGAACATCTCAGTGGCATAATTCGTTAGTTATTG  
       roLeuAspArgGluLeuSerGlnTrpHisAsnSerLeuValIleA  
  
 721 CTGCTGAAATCAACAATCCCAAAGAGACAACACGCGTGGCTGTTT  
       laAlaGluIleAsnAsnProLysGluThrThrArgValAlaValP  
  
 766 TTGTGAGAATTTTGGATGTTAATGACAATGCCCCACAGTTTGCTG  
       heValArgIleLeuAspValAsnAspAsnAlaProGlnPheAlaV  
  
 811 TGTTCATGACACTTTTGTATGTGAAAATGCCAGACCAGGGCAGC  
       alPheTyrAspThrPheValCysGluAsnAlaArgProGlyGlnL  
  
 856 TAATACAGACTATAAGTGCAGTAGACAAAGATGACCCTTTAGGTG  
       euIleGlnThrIleSerAlaValAspLysAspAspProLeuGlyG  
  
 901 GACAGAAATTTTTTTTTCAGTTTAGCTGCTGTCAATCCAAACTTCA  
       lyGlnLysPhePhePheSerLeuAlaAlaValAsnProAsnPheT  
  
 946 CAGTACAGGATAATGAAGATAATACTGCCAGAATCTTAACCAGAA  
       hrValGlnAspAsnGluAspAsnThrAlaArgIleLeuThrArgL

Fig. 4

10002050-110201

991 AAAATGGATTCAATAGACATGAAATCAGTACCTATCTCTTGCCCTG  
 ysAsnGlyPheAsnArgHisGluIleS rThrTyrLeuLeuProV  
 1036 TGGTGATATCAGACAATGATTACCCGATTGAGAGCAGCACAGGCA  
 alValIleSerAspAsnAspTyrProIleGlnSerSerThrGlyT  
 1081 CACTGACCATTTCGAGTGTGTGCTTGTGACAGCCAAGGCAACATGC  
 hrLeuThrIleArgValCysAlaCysAspSerGlnGlyAsnMetG  
 1126 AATCCTGCAGTGCTGAAGCCCTGCTCCTCCCTGCCGGCCTCAGCA  
 lnSerCysSerAlaGluAlaLeuLeuLeuProAlaGlyLeuSerT  
 1171 CTGGGGCCTTGATCGCCATCCTCCTCTGCATCATCATTCTACTGG  
 hrGlyAlaLeuIleAlaIleLeuLeuCysIleIleIleLeuLeuV  
 1216 TTATAGTAGTACTGTTTGCAGCTCTGAAAGGACAGCGAAAAAAG  
 alIleValValLeuPheAlaAlaLeuLysGlyGlnArgLysLysG  
 1261 AGCCTCTGATCTTGTCAAAGAAGATATCAGAGACAACATTGTGA  
 luProLeuIleLeuSerLysGluAspIleArgAspAsnIleValS  
 1306 GCTATAACGATGAGGGTGGTGGAGAGGAGGACACCCAGGCCTTTG  
 erTyrAsnAspGluGlyGlyGlyGluGluAspThrGlnAlaPheA  
 1351 ATATCGGCACCCTGAGGAATCCTGCAGCCATTGAGGAAAAAAGC  
 spIleGlyThrLeuArgAsnProAlaAlaIleGluGluLysLysL  
 1396 TCCGGCGAGATATTATTCCAGAAACGTTATTTATTCCTCGGAGGA  
 euArgArgAspIleIleProGluThrLeuPheIleProArgArgT  
 1441 CTCCTACAGCTCCAGATAACACGGACGTCCGGGATTTTCAATTAATG  
 hrProThrAlaProAspAsnThrAspValArgAspPheIleAsnG  
 1486 AAAGGCTAAAAGAGCATGATCTTGACCCACCGCACCCCCCTACG  
 luArgLeuLysGluHisAspLeuAspProThrAlaProProTyrA  
 1531 ACTCACTTGCAACCTATGCCTATGAAGGAAATGATTCCATTGCTG  
 spSerLeuAlaThrTyrAlaTyrGluGlyAsnAspSerIleAlaG  
 1576 AATCTCTGAGTTCATTAGAATCAGGTACTACTGAAGGAGACCAAA  
 luSerLeuSerSerLeuGluSerGlyThrThrGluGlyAspGlnA  
 1621 ACTACGATTACCTCCGAGAATGGGGCCCTCGGTTTAATAAGCTAG  
 snTyrAspTyrLeuArgGluTrpGlyProArgPheAsnLysLeuA  
 1666 CAGAAATGTATGGTGGTGGGGAAAGTGACAAAGACTCTTAACGTA  
 laGluMetTyrGlyGlyGlyGluSerAspLysAspSer  
 1711 GGATATATGTTCTGTTCAAACAAGAGAAAGTAACTCTACCCATGC  
 1756 TGTCTCCACTTCACAATATTTGATATTCAGGAGCATTTCCTGCAG  
 1801 TCAGCACAATTTTTTCTCA

Fig. 4 Continued

10002050-10201

1 CAAAGGCTGGAGACAAGTGGGTTGGGGGTTGGTTTTAATTTGGCA  
 46 GTTGTAAATTAATGGTCAATTTTAATAGTCCGTAATTGATGGCAGC  
 91 CTGCTGTGGTACATGTGTGAAAGATTATCACTTTGAATATACGGA  
 136 ATGTGATAGCAGTGGCTCCAGGTGGAGAGTTGCCATTCCAAATTC  
 181 TGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGCAAAGA  
  
 226 ATGCACTCTTCTTGGATCCCTCGTGGAACTACATAGAATCTAAT  
 MetHisSerSerTrpIleProArgGlyAsnTyrIleGluSerAsn  
  
 271 CGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAG  
 ArgAspAspCysThrValSerLeuIleTyrAlaValHisLeuLys  
  
 316 AAGTCAGGCTATGTCTTCTTTGAGTACCAGTATGTCGACAACAAC  
 LysSerGlyTyrValPhePheGluTyrGlnTyrValAspAsnAsn  
  
 361 ATCTTCTTTGAGTTCTTTATTCAAATGATCAGTGCCAGGAGATG  
 IlePhePheGluPhePheIleGlnAsnAspGlnCysGlnGluMet  
  
 406 GACACCACCACTGACAAGTGGGTAAACTTACAGACAATGGAGAA  
 AspThrThrThrAspLysTrpValLysLeuThrAspAsnGlyGlu  
  
 451 TGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTC  
 TrpGlySerHisSerValMetLeuLysSerGlyThrAsnIleLeu  
  
 496 TACTGGAGAACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAG  
 TyrTrpArgThrThrGlyIleLeuMetGlySerLysAlaValLys  
  
 541 CCTGTGCTGGTAAAAATATCACAATTGAAGGGGTGGCGTACACA  
 ProValLeuValLysAsnIleThrIleGluGlyValAlaTyrThr  
  
 586 TCAGAATGTTTTCTTGCAAGCCAGGCACATTCAGCAACAAACCA  
 SerGluCysPheProCysLysProGlyThrPheSerAsnLysPro  
  
 631 GGTTCATTCAACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAG  
 GlySerPheAsnCysGlnValCysProArgAsnThrTyrSerGlu  
  
 676 AAAGGAGCCAAAGAATGTATAAGGTGTAAAGACGACTCTCAATTT  
 LysGlyAlaLysGluCysIleArgCysLysAspAspSerGlnPhe  
  
 721 TCAGAGGAAGGATCCAGTGAGTGTACAGAGCGCCCTCCCTGTACC  
 SerGluGluGlySerSerGluCysThrGluArgProProCysThr  
  
 766 ACAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA  
 ThrLysAspTyrPheGlnIleHisThrProCysAspGluGluGly  
  
 811 AAGACACAGATAATGTACAAGTGGATAGAGCCCAAAATCTGCCGG  
 LysThrGlnIleMetTyrLysTrpIleGluProLysIleCysArg  
  
 856 GAGGATCTCACAGATGCTATTAGATTGCCCCCTTCTGGAGAGAAG  
 GluAspLeuThrAspAlaIleArgLeuProProSerGlyGluLys  
  
 901 AAGGATTGTCCGCCTTGCAACCCTGGATTTTATAACAATGGATCA  
 LysAspCysProProCysAsnProGlyPheTyrAsnAsnGlySer  
  
 946 TCTTCTTGCCATCCCTGTCCTCCTGGAACATTTTTCAGATGGAACC  
 S rSerCysHisProCysProProGlyThrPheS rAspGlyThr

Fig. 5

10002050 " 110201



991 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGC  
 LysGluCysArgProCysProAlaGlyThrGluProAlaLeuGly  
 1036 TTTGAATATAAATGGTGGAAATGTCCTTCCTGGCAACATGAAAAC  
 PheGluTyrLysTrpTrpAsnValLeuProGlyAsnMetLysThr  
 1081 TCCTGCTTCAATGTTGGGAATTCAAAGTCCGATGGAATGAATGGT  
 SerCysPheAsnValGlyAsnSerLysCysAspGlyMetAsnGly  
 1126 TGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT  
 TrpGluValAlaGlyAspHisIleGlnSerGlyAlaGlyGlySer  
 1171 GACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATTTAAA  
 AspAsnAspTyrLeuIleLeuAsnLeuHisIleProGlyPheLys  
 1216 CCACCAACATCTATGACTGGAGCCACGGGTCTGAACTAGGAAGA  
 ProProThrSerMetThrGlyAlaThrGlySerGluLeuGlyArg  
 1261 ATAACATTTGTCTTTGAGACCTCTGTTTCAGCTGACTGTGTTTTG  
 IleThrPheValPheGluThrLeuCysSerAlaAspCysvalLeu  
 1306 TACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA  
 TyrPheMetValAspIleAsnArgLysSerThrAsnValValGlu  
 1351 TCGTGGGGTGGAAACCAAGAAAAACAAGCTTACACCCATATCATC  
 SerTrpGlyGlyThrLysGluLysGlnAlaTyrThrHisIleIle  
 1396 TTCAAGAATGCAACTTTTACATTTACATGGGGCATTCCCAGAGAA  
 PheLysAsnAlaThrPheThrPheThrTrpGlyIleProArgGlu  
 1441 CTAATTCAGGGTCCAAGATAATAGACGGTTCCNCCATTGACATGT  
 LeuIleGlnGlyProArg  
 1486 TTGAAGGATTTATTCCTATTCAC

Fig. 5 Continued

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**Fig. 6**

901 TCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTC  
 SerAspCysTyrAlaGluGlnValValAlaArgValAlaArgVal  
 946 TGCAAGGGCGATATGGGGGGCGCACGGACCCTGCAGAGGAAGTGG  
 CysLysGlyAspMetGlyGlyAlaArgThrLeuGlnArgLysTrp  
 991 ACCACGTTCTGAAGGCGCGGCTGGCATGCTCTGCCCCGAACCTGG  
 ThrThrPheLeuLysAlaArgLeuAlaCysSerAlaProAsnTrp  
 1036 CAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGAC  
 GlnLeuTyrPheAsnGlnLeuGlnAlaMethisThrLeuGlnAsp  
 1081 ACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAG  
 ThrSerTrpHisAsnThrThrPhePheGlyValPheGlnAlaGln  
 1126 TGGGGTGACATGTACCTGTGCGCCATCTGTGAGTACCAGTTGGAA  
 TrpGlyAspMetTyrLeuSerAlaIleCysGluTyrGlnLeuGlu  
 1171 GAGATCCAGCGGGTGTGAGGGCCCCCTATAAGGAGTACCATGAG  
 GluIleGlnArgValPheGluGlyProTyrLysGluTyrHisGlu  
 1216 GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCT  
 GluAlaGlnLysTrpAspArgTyrThrAspProValProSerPro  
 1261 CGGCCTGGCTCGTGCATTAACAACCTGGCATCGGCGCCACGGCTAC  
 ArgProGlySerCysIleAsnAsnTrpHisArgArgHisGlyTyr  
 1306 ACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAG  
 ThrSerSerLeuGluLeuProAspAsnIleLeuAsnPheValLys  
 1351 AAGCACCCGCTGATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGC  
 LysHisProLeuMetGluGluGlnValGlyProArgTrpSerArg  
 1396 CCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC  
 ProLeuLeuValLysLysGlyThrAsnPheThrHisLeuValAla  
 1441 GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTC  
 AspArgValThrGlyLeuAspGlyAlaThrTyrThrValLeuPhe  
 1486 ATTGGCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGG  
 IleGlyThrGlyAspGlyTrpLeuLeuLysAlaValSerLeuGly  
 1531 CCCTGGGTTACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAG  
 ProTrpValHisLeuIleGluGluLeuGlnLeuPheAspGlnGlu  
 1576 CCCATGAGAAGCCTGGTGCTATCTCAGAGCAAGAAGCTGCTCTTT  
 ProMetArgSerLeuValLeuSerGlnSerLysLysLeuLeuPhe  
 1621 GCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC  
 AlaGlySerArgSerGlnLeuValGlnLeuProValAlaAspCys  
 1666 ATAAAGTATCGCTCCTGTGCAGACTGTGTCTCGCCCGGGACCCC  
 IleLysTyrArgSerCysAlaAspCysValLeuAlaArgAspPro

Fig. 6 Continued

10002050-110201

1711 TATTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGT  
TyrCysAlaTrpSerValAsnThrSerArgCysValAlaValGly  
1756 GGCCACTTTGGATCTTTACTGATCCAGCATGTGATGACCTCGGAC  
GlyHisPheGlySerLeuLeuIleGlnHisValMetThrSerAsp  
1801 ACTTCAGGCATTTGCAACCTCCGTGGCAGTAAGAAAGTCAGGCCC  
ThrSerGlyIleCysAsnLeuArgGlySerLysLysValArgPro  
1846 ACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGCTG  
ThrProLysAsnIleThrValValAlaGlyThrAspLeuValLeu  
1891 CCCTGCCACCTCTCCTCCACTTGGCCCCGGGGTTCAGTGGTATTT  
ProCysHisLeuSerSerThrTrpProArgGlySerValValPhe  
1936 TAAACTTGCCTTCTTCTGTACAGGGCTGGGAAAGGCTGTGTTAG  
1981 GGGAAAAAAGGAAAGGGTGGGCCTGCTGTGGACAATGGCATACT  
2026 CTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTGTAACCTTATTG  
2071 TGTCCCCGCGTATTTATTTGTTGTAAATATTTGAGTATTTTATA  
2116 TTGACAAATAAAATGGAGAAAATGAAAAAAAAAAAAAAAAA

Fig. 6 Continued

10002050-110201

Fig. 7

901 TCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTC  
 SerAspCysTyrAlaGluGlnValValAlaArgValAlaArgVal  
 946 TGCAAGGGCGATATGGGGGCGCACGGACCCTGCAGAGGAAGTGG  
 CysLysGlyAspMetGlyGlyAlaArgThrLeuGlnArgLysTrp  
 991 ACCACGTTCTTGAAGGCGCGGCTGGCATGCTCTGCCCCGAAGTGG  
 ThrThrPheLeuLysAlaArgLeuAlaCysSerAlaProAsnTrp  
 1036 CAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGAC  
 GlnLeuTyrPheAsnGlnLeuGlnAlaMetHisThrLeuGlnAsp  
 1081 ACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAG  
 ThrSerTrpHisAsnThrThrPhePheGlyValPheGlnAlaGln  
 1126 TGGGGTGACATGTACCTGTCGGCCATCTGTGAGTACCAGTTGGAA  
 TrpGlyAspMetTyrLeuSerAlaIleCysGluTyrGlnLeuGlu  
 1171 GAGATCCAGCGGGTGTGAGGGCCCTATAAGGAGTACCATGAG  
 GluIleGlnArgValPheGluGlyProTyrLysGluTyrHisGlu  
 1216 GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCT  
 GluAlaGlnLysTrpAspArgTyrThrAspProValProSerPro  
 1261 CGGCCTGGCTCGTGCATTAACAACCTGGCATCGGCGCCACGGCTAC  
 ArgProGlySerCysIleAsnAsnTrpHisArgArgHisGlyTyr  
 1306 ACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAG  
 ThrSerSerLeuGluLeuProAspAsnIleLeuAsnPheValLys  
 1351 AAGCACCCGCTGATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGC  
 LysHisProLeuMetGluGluGlnValGlyProArgTrpSerArg  
 1396 CCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC  
 ProLeuLeuValLysLysGlyThrAsnPheThrHisLeuValAla  
 1441 GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTC  
 AspArgValThrGlyLeuAspGlyAlaThrTyrThrValLeuPhe  
 1486 ATTGGCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGG  
 IleGlyThrGlyAspGlyTrpLeuLeuLysAlaValSerLeuGly  
 1531 CCCTGGGTTCACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAG  
 ProTrpValHisLeuIleGluGluLeuGlnLeuPheAspGlnGlu  
 1576 CCCATGAGAAGCCTGGTGCTATCTCAGAGCAAGAAGCTGCTCTTT  
 ProMetArgSerLeuValLeuSerGlnSerLysLysLeuLeuPhe  
 1621 GCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC  
 AlaGlySerArgSerGlnLeuValGlnLeuProValAlaAspCys  
 1666 ATAAAGTATCGCTCCTGTGCAGACTGTGTCCTCGCCCGGGACCCC  
 IleLysTyrArgSerCysAlaAspCysValLeuAlaArgAspPro

Fig. 7 Continued

1002050-10201

1711 TATTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGT  
TyrCysAlaTrpSerValAsnThrSerArgCysValAlaValGly

1756 GGCCACTTTGGATCTTTACTGATCCAGCATGTGATGACCTCGGAC  
GlyHisPheGlySerLeuLeuIleGlnHisValMetThrSerAsp

1801 ACTTCAGGCATTTGCAACCTCCGTGGCAGTAAGATACAGTCAGGC  
ThrSerGlyIleCysAsnLeuArgGlySerLysIleGlnSerGly

1846 CCACTNCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTG  
ProLeuProLysAsnIleThrValValAlaGlyThrAspLeuVal

1891 CTGCCCTGCCACCTCTCCTCCAACCTGGCCCTGCCCCGACTCCAAC  
LeuProCysHisLeuSerSerAsnLeuAlaLeuProAspSerAsn

1936 CCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCGTCGGCGG  
ProGluGluSerSerVal

1981 ANAGCGTGGGAGGTGTAGCTCCTACTTTTGCACAGGCACCAGCTA  
2026 TCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGGGACAGATAC  
2071 TGCCCAGCACCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACG  
2116 GGCACCTGCACTTGGTGTGGTCACCAGGGCACCAGCTCGCAGAAGG  
2161 CATCTTCCTCCTCTCTGTGAATCACAGACACGCGGGACCCAGCC  
2206 GCCAAAATTTTCAAGGCAGAAAGTTNAAGATGTGTGTTTGNTGTAT  
2251 TTGACATGTGTTTGTGTGTGTGTGTATGTGTGTG

Fig. 7 Continued

1002050-10201

1 ACCGACGTCGAATATCCATGCATCCGCGTGCAGGTGGCAGACGGA  
 46 CTCCGGCGGAATGGGGGGTGTGGCTGCTCCGCCAGGGTCCCCAGG  
 91 GTGGGAGAGCGGCTCCGCGGCCACCGATGCCCGGACCCCCCTCTGT  
  
 136 CTTCTGCTAGACATGCTCTTCTCTCGTTTCATGCAGGCTCTTGG  
     MetLeuPheLeuSerPheHisAlaGlySerTrp  
  
 181 GAAAGCTGGTGCTGCTGCTGCCTGATTCCCGCCGACAGACCTTGG  
     GluSerTrpCysCysCysCysLeuIleProAlaAspArgProTrp  
  
 226 GACCGGGGCCAACACTGGCAGCTGGAGATGGCGGACACGAGATCC  
     AspArgGlyGlnHisTrpGlnLeuGluMetAlaAspThrArgSer  
  
 271 GTGCACGAGACTAGGTTTGAGGCGGCCGTGAAGGTGATCCAGAGT  
     ValHisGluThrArgPheGluAlaAlaValLysValIleGlnSer  
  
 316 TTGCCGAAGAATGGTTCATTCCAGCCAACAAATGAAATGATGCTT  
     LeuProLysAsnGlySerPheGlnProThrAsnGluMetMetLeu  
  
 361 AAATTTTATAGCTTCTATAAGCAGGCAACTGAAGGACCCTGTAA  
     LysPheTyrSerPheTyrLysGlnAlaThrGluGlyProCysLys  
  
 406 CTTTCAAGGCCTGGATTTTGGGATCCTATTGGAAGATATAAATGG  
     LeuSerArgProGlyPheTrpAspProIleGlyArgTyrLysTrp  
  
 451 GATGCTTGGAGTTCACTGGGTGATATGACCAAAGAGGAAGCCATG  
     AspAlaTrpSerSerLeuGlyAspMetThrLysGluGluAlaMet  
  
 496 ATTGCATATGTTGAAGAAATGAAAAAGATTATTGAAACTATGCCA  
     IleAlaTyrValGluGluMetLysLysIleIleGluThrMetPro  
  
 541 ATGACTGAGAAAGTTGAAGAATTGCTGCGTGTGCATAGGTCCATTT  
     MetThrGluLysValGluGluLeuLeuArgValIleGlyProPhe  
  
 586 TATGAAATTGTCGAGGACAAAAAGAGTGGCAGGAGTTCTGATATA  
     TyrGluIleValGluAspLysLysSerGlyArgSerSerAspIle  
  
 631 ACCTCAGTCCGACTGGAGAAAATCTCTAAATGTTTAGAAGATCTT  
     ThrSerValArgLeuGluLysIleSerLysCysLeuGluAspLeu  
  
 676 GGTAATGTTCTCACTTCTACTCCAAACGCCAAAACCGTTAATGGT  
     GlyAsnValLeuThrSerThrProAsnAlaLysThrValAsnGly  
  
 721 AAAGCTGAAAGCAGTGACAGTGGAGCCGAGTCTGAGGAAGAAGAG  
     LysAlaGluSerSerAspSerGlyAlaGluSerGluGluGluGlu  
  
 766 GCCCAAGAAGAAGTGAAAGGAGCAGAACAAAGTGATAATGATAAG  
     AlaGlnGluGluValLysGlyAlaGluGlnSerAspAsnAspLys  
  
 811 AAAATGATGAAGAAGTCAGCAGACCATAAGAATTTGGAAGTCATT  
     LysMetMetLysLysSerAlaAspHisLysAsnLeuGluValIle

Fig. 8



856 GTCAC TAATGGCTATGATAAAGATGGCTTTGTT CAGGATATACAG  
 ValThrAsnGlyTyrAspLysAspGlyPheValGlnAspIleGln  
 901 AATGACATTCATGCCAGTTCTTCCCTGAATGGCAGAAGCACTGAA  
 AsnAspIleHisAlaSerSerSerLeuAsnGlyArgSerThrGlu  
 946 GAAGTAAAGCCCATTGATGAAAAC TTGGGGCAAAC TGGAAAATCT  
 GluValLysProIleAspGluAsnLeuGlyGlnThrGlyLysSer  
 991 GCTGTTTGCATTACCAAGATATAAATGATGATCATGTTGAAGAT  
 AlaValCysIleHisGlnAspIleAsnAspAspHisValGluAsp  
 1036 GTTACAGGAATTCAGCATTTGACAAGCGATT CAGACAGTGAAGTT  
 ValThrGlyIleGlnHisLeuThrSerAspSerAspSerGluVal  
 1081 TACTGTGATTCTATGGAACAATTTGGACAAGAAGAGTCTTTAGAC  
 TyrCysAspSerMetGluGlnPheGlyGlnGluGluSerLeuAsp  
 1126 AGCTTTACGTCCAACAATGGACCATTT CAGTATTACTTGGGTGGT  
 SerPheThrSerAsnAsnGlyProPheGlnTyrTyrLeuGlyGly  
 1171 CATTCCAGTCAACCCATGGAAAATTCTGGATTTCGTGAAGATATT  
 HisSerSerGlnProMetGluAsnSerGlyPheArgGluAspIle  
 1216 CAAGTACCTCCTGGAAATGGCAACATTGGGAATATGCAGGTGGTT  
 GlnValProProGlyAsnGlyAsnIleGlyAsnMetGlnValVal  
 1261 GCAGTTGAAGGAAAAGGTGAAGTCAAGCATGGAGGAGAAGATGGC  
 AlaValGluGlyLysGlyGluValLysHisGlyGlyGluAspGly  
 1306 AGGAATAACAGCGGAGCACCACACCGGGAGAAGCGAGGCGGAGAA  
 ArgAsnAsnSerGlyAlaProHisArgGluLysArgGlyGlyGlu  
 1351 ACTGACGAATTCTCTAATGTTAGAAGAGGAAGAGGACATAGGATG  
 ThrAspGluPheSerAsnValArgArgGlyArgGlyHisArgMet  
 1396 CAACACTTGAGCGAAGGAACCAAGGGCCGGCAGGTGGGAAGTGGAA  
 GlnHisLeuSerGluGlyThrLysGlyArgGlnValGlySerGly  
 1441 GGTGATGGGGAGCGCTGGGGCTCCGACAGAGGGTCCCCGAGGCAGC  
 GlyAspGlyGluArgTrpGlySerAspArgGlySerArgGlySer  
 1486 CTCAATGAGCAGATCGCCCTCGTGCTGATGAGACTGCAGGAGGAC  
 LeuAsnGluGlnIleAlaLeuValLeuMetArgLeuGlnGluAsp  
 1531 ATGCAGAATGTCCTTCAGAGACTGCAGAAACTGGAAATGCTGACT  
 MetGlnAsnValLeuGlnArgLeuGlnLysLeuGluMetLeuThr  
 1576 GCTTTGCAGGCAAAATCATCAACATCAACATTGCAGACTGCTCCT  
 AlaLeuGlnAlaLysSerSerThrSerThrLeuGlnThrAlaPro  
 1621 CAGCCACCTCACAGAGACCATCTTGGTGGCCCTTCGAGATGTCT  
 GlnProThrS rGlnArgProSerTrpTrpProPheGluMetS r

Fig. 8 Continued

T020T " 052000T

1666 CCTGGTGTGCTAACGTTTGCCATCATATGGCCTTTTATTGCACAG  
ProGlyValLeuThrPheAlaIleIleTrpProPheIleAlaGln

1711 TGGTTGGTGTATTTATACTATCAAAGAAGGAGAAGAAAACCTGAAC  
TrpLeuValTyrLeuTyrTyrGlnArgArgArgArgLysLeuAsn

1756 TGAGGGAAAATGGTGTTCCTCAAGAAGACTACTGGAACCTGGAT  
1801 GACCTCAGAATGAACTGGATTGTGGTGTTCACAAGAAAATCTTAG  
1849 TTTGTGATGATTACATTGCTTTTGTGTCCNGTAGTTTAGTTTG  
1891 TGTACATATATACACATATATATTTTGCCTACACAAACG

Fig. 8 Continued

10002050-110201

1 CATTCTAGCTGCCTGCTGCCTCCGCAGCGTCCCCCAGCTCTCCC  
 46 TGTGCTAACTGCCTGCACCTTGGACAGAGCGGGTGCACAAATCAG  
 91 AAGGATTAGTTGGGACCTGCCTTGGCGACCCCATGGCATCCCCCA  
 MetAlaSerProA  
 136 GAACCGTAACTATTGTGGCCCTCTCAGTGGCCCTGGGACTCTTCT  
 rgThrValThrIleValAlaLeuSerValAlaLeuGlyLeuPheP  
 181 TTGTTTTTCATGGGGACTATCAAGCTGACCCCCAGGCTCAGCAAGG  
 heValPheMetGlyThrIleLysLeuThrProArgLeuSerLysA  
 226 ATGCCTACAGTGAGATGAAACGTGCTTACAAGAGCTATGTTGAG  
 spAlaTyrSerGluMetLysArgAlaTyrLysSerTyrValArgA  
 271 CCCTCCCTCTGCTGAAGAAAATGGGGATCAATTCCATTCTCCTCC  
 laLeuProLeuLeuLysLysMetGlyIleAsnSerIleLeuLeuA  
 316 GAAAAAGCATTGGTGCCCTTGAAGTGGCCTGTGGCATCGTCATGA  
 rgLysSerIleGlyAlaLeuGluValAlaCysGlyIleValMetT  
 361 CCCTTGCTGCCTGGGCGTCCCAAAGATGTGGCCAACTTCTTCCTAC  
 hrLeuValProGlyArgProLysAspValAlaAsnPhePheLeuL  
 406 TGTTGCTGGTGTGGCTGTGCTCTTCTTCCACCAGCTGGTCGGTG  
 euLeuLeuValLeuAlaValLeuPhePheHisGlnLeuValGlyA  
 451 ATCCTCTCAAACGCTACGCCCATGCTCTGGTGTTTGAATCCTGC  
 spProLeuLysArgTyrAlaHisAlaLeuValPheGlyIleLeuL  
 496 TCACTTGCCGCCTGCTGATTGCTCGCAAGCCCGAAGACCGGTCTT  
 euThrCysArgLeuLeuIleAlaArgLysProGluAspArgSerS  
 541 CTGAGAAGAAGCCTTTGCCAGGGAATGCTGAGGAGCAACCTCCT  
 erGluLysLysProLeuProGlyAsnAlaGluGluGlnProSerL  
 586 TATATGAGAAGGCCCTCAGGGCAAAGTGAAGGTGTCATAGAAAA  
 euTyrGluLysAlaProGlnGlyLysValLysValSer

Fig. 9

10002050-110201



991 TACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGA  
 sThrThrLysAspTyrPheGlnIleHisThrProCysAspGluGl  
 1036 AGGAAAGACACAGATAATGTACAAGTGGATAGAGCCCAAATCTG  
 uGlyLysThrGlnIleMetTyrLysTrpIleGluProLysIleCy  
 1081 CCGGGAGGATCTCACAGATGCTATTAGATTGCCCCCTTCTGGAGA  
 sArgGluAspLeuThrAspAlaIleArgLeuProProSerGlyGl  
 1126 GAAGAAGGATTGTCCGCCTTGCAACCCTGGATTTTATAACAATGG  
 uLysLysAspCysProProCysAsnProGlyPheTyrAsnAsnGl  
 1171 ATCATCTTCTTGCCATCCCTGTCCTCCTGGAACATTTTCAGATGG  
 ySerSerSerCysHisProCysProProGlyThrPheSerAspGl  
 1216 AACCAGGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACT  
 yThrLysGluCysArgProCysProAlaGlyThrGluProAlaLe  
 1261 TGGCTTTGAATATAAATGGTGAATGTCCTTCCTGGCAACATGAA  
 uGlyPheGluTyrLysTrpTrpAsnValLeuProGlyAsnMetLy  
 1306 AACTTCCTGCTTCAATGTTGGAATTCAAAGTGCATGGAATGAA  
 sThrSerCysPheAsnValGlyAsnSerLysCysAspGlyMetAs  
 1351 TGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGG  
 nGlyTrpGluValAlaGlyAspHisIleGlnSerGlyAlaGlyGl  
 1396 TTCTGACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATT  
 ySerAspAsnAspTyrLeuIleLeuAsnLeuHisIleProGlyPh  
 1441 TAAACCACCAACATCTATGACTGGAGCCACGGGTTCTGAACTAGG  
 eLysProProThrSerMetThrGlyAlaThrGlySerGluLeuGl  
 1486 AAGAATAACATTTGTCTTTGAGACCCTCTGTTTCAGCTGACTGTGT  
 yArgIleThrPheValPheGluThrLeuCysSerAlaAspCysVa  
 1531 TTTGTACTIONCATGGTGGATATTAATAGAAAAAGTACAAATGTGGT  
 lLeuTyrPheMetValAspIleAsnArgLysSerThrAsnValVa  
 1576 AGAATCGTGGGGTGAACCAAAGAAAAACAAGCTTACACCCATAT  
 lGluSerTrpGlyGlyThrLysGluLysGlnAlaTyrThrHisIl  
 1621 CATCTTCAAGAATGCAACTTTTACATTTACATGGGGCATTCCAG  
 eIlePheLysAsnAlaThrPheThrPheThrTrpGlyIleProAr  
 1666 AGAACTAATTCAGGGTCCAAGATAATAGACGGTTCCNCCATTGAC  
 gGluLeuIleGlnGlyProArg  
 1711 ATGTTTGAAGGATTTATTCCTATTAC

Fig. 10 Continued

10002050.10201

Fig. 11

901 TCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTC  
 SerAspCysTyrAlaGluGlnValValAlaArgValAlaArgVal  
 946 TGCAAGGGCGATATGGGGGGCGCACGGACCCTGCAGAGGAAGTGG  
 CysLysGlyAspMetGlyGlyAlaArgThrLeuGlnArgLysTrp  
 991 ACCACGTTCTGAAGGCGGGCTGGCATGCTCTGCCCCGAAGTGG  
 ThrThrPheLeuLysAlaArgLeuAlaCysSerAlaProAsnTrp  
 1036 CAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGAC  
 GlnLeuTyrPheAsnGlnLeuGlnAlaMetHisThrLeuGlnAsp  
 1081 ACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAG  
 ThrSerTrpHisAsnThrThrPhePheGlyValPheGlnAlaGln  
 1126 TGGGGTGACATGTACCTGTCTGGCCATCTGTGAGTACCAGTTGGAA  
 TrpGlyAspMetTyrLeuSerAlaIleCysGluTyrGlnLeuGlu  
 1171 GAGATCCAGCGGGTGTGAGGGCCCCCTATAAGGAGTACCATGAG  
 GluIleGlnArgValPheGluGlyProTyrLysGluTyrHisGlu  
 1216 GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCT  
 GluAlaGlnLysTrpAspArgTyrThrAspProValProSerPro  
 1261 CGGCCTGGCTCGTGCATTAACAAGTGGCATCGGCGCCACGGCTAC  
 ArgProGlySerCysIleAsnAsnTrpHisArgArgHisGlyTyr  
 1306 ACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAG  
 ThrSerSerLeuGluLeuProAspAsnIleLeuAsnPheValLys  
 1351 AAGCACCCGCTGATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGC  
 LysHisProLeuMetGluGluGlnValGlyProArgTrpSerArg  
 1396 CCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC  
 ProLeuLeuValLysLysGlyThrAsnPheThrHisLeuValAla  
 1441 GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTC  
 AspArgValThrGlyLeuAspGlyAlaThrTyrThrValLeuPhe  
 1486 ATTGGCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGG  
 IleGlyThrGlyAspGlyTrpLeuLeuLysAlaValSerLeuGly  
 1531 CCCTGGGTTCACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAG  
 ProTrpValHisLeuIleGluGluLeuGlnLeuPheAspGlnGlu  
 1576 CCCATGAGAAGCCTGGTGTCTATCTCAGAGCAAAAAGCTGCTCTTT  
 ProMetArgSerLeuValLeuSerGlnSerLysLysLeuLeuPhe  
 1621 GCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCCGTGGCCGACTGC  
 AlaGlySerArgSerGlnLeuValGlnLeuProValAlaAspCys  
 1666 ATTAAGTATCGCTCCTGTGCAGACTGTGTCCTCGCCCGGGACCCC  
 IleLysTyrArgSerCysAlaAspCysValLeuAlaArgAspPro

Fig. 11 Continued

10002050-110201

1711 TATTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGT  
TyrCysAlaTrpSerValAsnThrSerArgCysValAlaValGly  
1756 GGCCACTCTGGATCTCTACTGATCCAGCATGTGATGACCTCGGAC  
GlyHisSerGlySerLeuLeuIleGlnHisValMetThrSerAsp  
1801 ACTTCAGGCATCTGCAACCTCCGTGGCAGTAAGAAAGTCAGGCCC  
ThrSerGlyIleCysAsnLeuArgGlySerLysLysValArgPro  
1846 ACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGCTG  
ThrProLysAsnIleThrValValAlaGlyThrAspLeuValLeu  
1891 CCCTGCCACCTCTCCTCCACTTGGCCCCGGGGTTCAGTGGTATTT  
ProCysHisLeuSerSerThrTrpProArgGlySerValValPhe  
1936 TATACTTGCTTCTTCTGTACAGGGCTGGGAAAGGCTGTGTGAG  
TyrThrCysLeuLeuProValGlnGlyTrpGluArgLeuCysGlu  
1981 GGGAAAAAAGGAAAGGGTGGGCCTGCTGTGGACAATGGCATACT  
GlyLysLysArgLysGlyTrpAlaCysCysGlyGlnTrpHisThr  
2026 CTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTGTAACCTATTG  
LeuPheGlnPro  
2071 TGTCCCCGCGTATTTATTTGTTGTAAATATTTGAGTATTTTTATA  
2116 TTGACAAATAAAATGGAGAAAATGAAAAAAAAAAAAAAAAAAAA

Fig. 11 Continued

10002050-110201



1 CGCTCCATGTATNAGTTTTCATGCAGGCTCTTGGGAAAGCTGGTGC  
 MetTyr---PheHisAlaGlySerTrpGluSerTrpCys  
 46 TGCTGCTGCCTGATTCCCGCCGACAGACCTTGGGACCGGGGCCAA  
 CysCysCysLeuIleProAlaAspArgProTrpAspArgGlyGln  
 91 CACTGGCAGCTGGAGATGGCGGACACGAGATCCGTGCACGAGACT  
 HisTrpGlnLeuGluMetAlaAspThrArgSerValHisGluThr  
 136 AGGTTTGAGGCGGCCGTGAAGGTGATCCAGAGTTTGCCGAAGAAT  
 ArgPheGluAlaAlaValLysValIleGlnSerLeuProLysAsn  
 181 GATTCATTCCAGCCAACAAATGAAATGATGCTTAAATTTTATAGC  
 AspSerPheGlnProThrAsnGluMetMetLeuLysPheTyrSer  
 226 TTCTATAAGCAGGCAACTGAAGGACCCTGTAACTTTCAAGGCCT  
 PheTyrLysGlnAlaThrGluGlyProCysLysLeuSerArgPro  
 271 GGATTTTGGGATCCTATTGGAAGATATAAATGGGATGCTTGGAGT  
 GlyPheTrpAspProIleGlyArgTyrLysTrpAspAlaTrpSer  
 316 TCACTGGGTGATATGACCAAAGAGGAAGCCATGATTGCATATGTT  
 SerLeuGlyAspMetThrLysGluGluAlaMetIleAlaTyrVal  
 361 GAAGAAATGAAAAAGATTATTGAAACTATGCCAATGACTGAGAAA  
 GluGluMetLysLysIleIleGluThrMetProMetThrGluLys  
 406 GTTGAAGAATTGCTGCGTGTCATAGGTCCATTTTATGAAATTGTC  
 ValGluGluLeuLeuArgValIleGlyProPheTyrGluIleVal  
 451 GAGGACAAAAAGAGTGGCAGGAGTTCTGATATAACCTCAGTCCGA  
 GluAspLysLysSerGlyArgSerSerAspIleThrSerValArg  
 496 CTGGAGAAAATCTCTAAATGTTTAGAAGATCTTGGTAATGTTCTC  
 LeuGluLysIleSerLysCysLeuGluAspLeuGlyAsnValLeu  
 541 ACTTCTACTCCAAACGCCAAAACCGTTAATGGTAAAGCTGAAAGC  
 ThrSerThrProAsnAlaLysThrValAsnGlyLysAlaGluSer  
 586 AGTGACAGTGGAGCCGAGTCTGAGGAAGAAGAGGCCCAAGAAGAA  
 SerAspSerGlyAlaGluSerGluGluGluGluAlaGlnGluGlu  
 631 GTGAAAGGAGCAGAACAAAGTGATAATGATAAGAAAATGATGAAG  
 ValLysGlyAlaGluGlnSerAspAsnAspLysLysMetMetLys  
 676 AAGTCAGCAGACCATAAGAATTTGGAAGTCATTGTCACTAATGGC  
 LysSerAlaAspHisLysAsnLeuGluValIleValThrAsnGly  
 721 TATGATAAAGATGGCTTTGTTCAGGATATACAGAATGACATTCAT  
 TyrAspLysAspGlyPheValGlnAspIleGlnAsnAspIleHis  
 766 GCCAGTTCTTCCCTGAATGGCAGAAGCACTGAAGAAGTAAAGCCC  
 AlaS rSerSerLeuAsnGlyArgSerThrGluGluValLysPro

Fig. 12

10002050-110201

811 ATTGATGAAAACCTTGGGGCAAACCTGGAAAATCTGCTGTTTGCATT  
 IleAspGluAsnLeuGlyGlnThrGlyLysSerAlaValCysIle  
 856 CACCAAGATATAAATGATGATCATGTTGAAGATGTTACAGGAATT  
 HisGlnAspIleAsnAspAspHisValGluAspValThrGlyIle  
 901 CAGCATTTGACAAGCGATTTCAGACAGTGAAGTTTACTGTGATTCT  
 GlnHisLeuThrSerAspSerAspSerGluValTyrCysAspSer  
 946 ATGGAACAATTTGGACAAGAAGAGTCTTTAGACAGCTTTACGTCC  
 MetGluGlnPheGlyGlnGluGluSerLeuAspSerPheThrSer  
 991 AACAAATGGACCATTTCAGTATTACTTGGGTGGTCATTCCAGTCAA  
 AsnAsnGlyProPheGlnTyrTyrLeuGlyGlyHisSerSerGln  
 1036 CCCATGGAAAATTCTGGATTTTCGTGAAGATATTCAAGTACCTCCT  
 ProMetGluAsnSerGlyPheArgGluAspIleGlnValProPro  
 1081 GGAAATGGCAACATTGGGAATATGCAGGTGGTTGCAGTTGAAGGA  
 GlyAsnGlyAsnIleGlyAsnMetGlnValValAlaValGluGly  
 1126 AAAGGTGAAGTCAAGCATGGAGGAGAAGATGGCAGGAATAACAGC  
 LysGlyGluValLysHisGlyGlyGluAspGlyArgAsnAsnSer  
 1171 GGAGCACCACACCGGGAGAAGCGAGGCGGAGAACTGACGAATTC  
 GlyAlaProHisArgGluLysArgGlyGlyGluThrAspGluPhe  
 1216 TCTAATGTTAGAAGAGGAAGAGGACATAGGATGCAACACTTGAGC  
 SerAsnValArgArgGlyArgGlyHisArgMetGlnHisLeuSer  
 1261 GAAGGAACCAAGGGCCGGCAGGTGGGAAGTGGAGGTGATGGGGAG  
 GluGlyThrLysGlyArgGlnValGlySerGlyGlyAspGlyGlu  
 1306 CGCTGGGGCTCCGACAGAGGGTCCCGAGGCAGCCTCAATGAGCAG  
 ArgTrpGlySerAspArgGlySerArgGlySerLeuAsnGluGln  
 1351 ATCGCCCTCGTGCTGATGAGACTGCAGGAGGACATGCAGAATGTC  
 IleAlaLeuValLeuMetArgLeuGlnGluAspMetGlnAsnVal  
 1396 CTTTCAGAGACTGCAGAACTGGAAACGCTGACTGCTTTGCAGGCA  
 LeuGlnArgLeuGlnLysLeuGluThrLeuThrAlaLeuGlnAla  
 1441 AAATCATCAACATCAACATTGCAGACTGCTCCTCAGCCCACCTCA  
 LysSerSerThrSerThrLeuGlnThrAlaProGlnProThrSer  
 1486 CAGAGACCATCTTGGTGGCCCTTCGAGATGTCTCCTGGTGTGCTA  
 GlnArgProSerTrpTrpProPheGluMetSerProGlyValLeu  
 1531 ACGTTTGCCATCATATGGCCTTTTATTGCACAGTGGTTGGTGTAT  
 ThrPheAlaIleIleTrpProPheIleAlaGlnTrpLeuValTyr

Fig. 12 Continued

10002050-110201

1576 TTATACTATCAAAGAAGGAGAAGAAAACCTGAACTGAGGAAAATGG  
LeuTyrTyrGlnArgArgArgArgLysLeuAsn  
1621 TGTTCCTCAAGAAGACTACTGGAACCTGGATGACCTCAGAATGA  
1666 ACTGGATTGTGGTGTTCAAGAAAATCTTAGTTTGTGATGATTA  
1711 CATTGCTTTTGTGTCCAGTAGTTTAGTTTGTGTACATATATAC  
1756 ACATATATATTTGCACTACACAAACGATAACATTTTAAGGACTA  
1801 ATATTGCTGATACTTGAATAATCAATCTCTACTAGGTTATAAGTA  
1846 GTATACACAGATTTACCCTGCCCTTGAACCTGAAGGACATTAAAT  
1891 TATTAATGATCATTTGGTAACATGTTTACCTGATTATCTTCATA  
1936 GAGTAACATAAGCTGCTTTTCAAAGGTACCATTGTGATAATGAGA  
1981 TCAAATTTATAAGTTATTATTTTAAATTTCTAAATTAAATAAAA  
2026 GAAAGAATGCAAAAAAAAAAAAAAAAAAAAAA

Fig. 12 Continued

10002050-110201

20936375-0-104: 1 ..MYXFHAGSWESWCCCCCLIPADRPWDRGQHWQLEMADTRSVHETRFEAA 48  
 |||||  
 20936375.0.1: 1 MLFLSFHAGSWESWCCCCCLIPADRPWDRGQHWQLEMADTRSVHETRFEAA 50

49 VKVIQSLPKNDSFQPTNEMMLKFYSFYKQATEGPCKLSRPGFWDPIGRYK 98  
 |||||  
 51 VKVIQSLPKNGSFQPTNEMMLKFYSFYKQATEGPCKLSRPGFWDPIGRYK 100

99 WDAWSSLGDMTKEEAMIAIYVEEMKKIIETMPMTEKVEELLRVIGPFYEIV 148  
 |||||  
 101 WDAWSSLGDMTKEEAMIAIYVEEMKKIIETMPMTEKVEELLRVIGPFYEIV 150

149 EDKKSGRSSDITSVRLEKISKCLEDLGNVLTSTPNAKTVNGKAESSDSGA 198  
 |||||  
 151 EDKKSGRSSDITSVRLEKISKCLEDLGNVLTSTPNAKTVNGKAESSDSGA 200

199 ESEEEEAQEEVKGAEQSDNDKKMMKKSADHKNLEVIVTNGYDKDGFVQDI 248  
 |||||  
 201 ESEEEEAQEEVKGAEQSDNDKKMMKKSADHKNLEVIVTNGYDKDGFVQDI 250

249 QNDIHASSSLNGRSTEEVKPIDENLGQTGKSAVCIHQDINDDHVEDVTGI 298  
 |||||  
 251 QNDIHASSSLNGRSTEEVKPIDENLGQTGKSAVCIHQDINDDHVEDVTGI 300

299 QHLTSDSDSEVYCDSEMEQFGQEEESLDSFTSNNGPFQYYLGGHSSQPMENS 348  
 |||||  
 301 QHLTSDSDSEVYCDSEMEQFGQEEESLDSFTSNNGPFQYYLGGHSSQPMENS 350

349 GFREDIQVPPGNGNIGNMQVVAVEGKGEVKHGGEDGRNNSGAPHREKRG 398  
 |||||  
 351 GFREDIQVPPGNGNIGNMQVVAVEGKGEVKHGGEDGRNNSGAPHREKRG 400

399 ETDEFSNVRRGRGRMQHLSEGTKGRQVGSGGDGERWGSDRGSRGSLNEQ 448  
 |||||  
 401 ETDEFSNVRRGRGRMQHLSEGTKGRQVGSGGDGERWGSDRGSRGSLNEQ 450

449 IALVLMRLQEDMQNVLQRLQKLETLTALQAKSSTSTLQTAPQPTSQRPSW 498  
 |||||  
 451 IALVLMRLQEDMQNVLQRLQKLEMLTALQAKSSTSTLQTAPQPTSQRPSW 500

499 WPFEMSPGVLTFAIWPFIAQWLVLVYLYYQRRRRKLN 534  
 |||||  
 501 WPFEMSPGVLTFAIWPFIAQWLVLVYLYYQRRRRKLN 536

Fig. 13

10002050.110201



FOOT" 0502000T

Sequences analyzed:

1. 20422974-0-132-ext-2\_Cura\_56
2. Q64151\_SEMAPHORIN\_4C\_PREC\_Mus
3. Q92854\_SEMAPHORIN
4. 20422974.2\_Cura\_54
5. 20422974.0.132\_Cura\_54

204229740132ext2_cura_56	MAPHWAVMLTFAARLWGLGIGAEVMMNLVPRKTVSSGELATVARRFSOTGIQDPRFLHLLTE
204229740132_cura_54	MAPHWAVMLTFAARLWGLGIGAEVMMNLVPRKTVSSGELATVARRFSOTGIQDPRFLHLLTE
204229742_cura_54	MAPHWAVMLTFAARLWGLGIGAEVMMNLVPRKTVSSGELATVARRFSOTGIQDPRFLHLLTE
q64151 semaphorin_4c_prec_mus	MAPHWAVMLTFAARLWGLGIGAEVMMNLVPRKTVSSGELATVARRFSOTGIQDPRFLHLLTE
q92854 semaphorin	VRMCTPRGELMALAYMFGTALAPAPDPRIMWEHREYHLV..QFHEPDIYNSALDLESE
204229740132ext2_cura_56	PTGELNAGARDAALFAF.SMEAFBELFOGATISWEAPAVEKKTKECTOKGKNNOTECEPNFTRRFLOP
204229740132_cura_54	PTGELNAGARDAALFAF.SMEAFBELFOGATISWEAPAVEKKTKECTOKGKNNOTECEPNFTRRFLOP
204229742_cura_54	PTGELNAGARDAALFAF.SMEAFBELFOGATISWEAPAVEKKTKECTOKGKNNOTECEPNFTRRFLOP
q64151 semaphorin_4c_prec_mus	HSGLNAGARDAALFAF.SYDAPBELFOGATISWEAPAVEKKTKECTOKGKNNOTECEPNFTRRFLOP
q92854 semaphorin	DKDTLYGAREAVFAVNAVNISEKQHEVYMKVSEDPKAKCAKCAKSKOTECLNYIRVLQOP
204229740132ext2_cura_56	YNASHLVCCGTAFOPKCTAVANMLTPTLFEHGEFFEDGKKGCPADDPKAGHAGLLVDGELYSA
204229740132_cura_54	YNASHLVCCGTAFOPKCTAVANMLTPTLFEHGEFFEDGKKGCPADDPKAGHAGLLVDGELYSA
204229742_cura_54	YNASHLVCCGTAFOPKCTAVANMLTPTLFEHGEFFEDGKKGCPADDPKAGHAGLLVDGELYSA
q64151 semaphorin_4c_prec_mus	YNSSHVAVCGTVAFOPKCTAVANMLTPTLFEHGEFFEDGKKGCPADDPKAGHAGLLVDGELYSA
q92854 semaphorin	LSAVISLVAVCGTNAFOPAQGDHINLTSEKF.LGKNEDDGKKGCPADDPKAGHAGLLVDGELYSG
204229740132ext2_cura_56	TEANNLEGTPEPTELRNMGPHHSMTKTEYTAATWENEPHIVGSAVAPESVGSFTGDDDDKVAFFFF
204229740132_cura_54	TEANNLEGTPEPTELRNMGPHHSMTKTEYTAATWENEPHIVGSAVAPESVGSFTGDDDDKVAFFFF
204229742_cura_54	TEANNLEGTPEPTELRNMGPHHSMTKTEYTAATWENEPHIVGSAVAPESVGSFTGDDDDKVAFFFF
q64151 semaphorin_4c_prec_mus	TEANNLEGTPEPTELRNMGPHHSMTKTEYTAATWENEPHIVGSAVAPESVGSFTGDDDDKVAFFFF
q92854 semaphorin	TISYNLEGTSEPTLSRN.SSHSPRTHENATPWENEPSEVFAADVIRKSPDSDPDGDDKVAFFFF
204229740132ext2_cura_56	RERAVESDCAVABEQAVARVARVCKGDVGGCARTLQORKWTFPELKARFACGSAPNWQINVENOLOA
204229740132_cura_54	RERAVESDCAVABEQAVARVARVCKGDVGGCARTLQORKWTFPELKARFACGSAPNWQINVENOLOA
204229742_cura_54	RERAVESDCAVABEQAVARVARVCKGDVGGCARTLQORKWTFPELKARFACGSAPNWQINVENOLOA
q64151 semaphorin_4c_prec_mus	SERAVEYDCVASEONAVARVARVCKGDVGGCARTLQORKWTFPELKARFACGSAPNWQINVENOLOA
q92854 semaphorin	TEVSVEYEFVFRVLTPRPARVCKEDQGGERTLQORKWTFPELKARFACSRPDSGIVENVERD

Fig. 15A

20020603 110000

204229740132ext2\_cura\_56  
204229740132\_cura\_54  
204229742\_cura\_54  
q64151 semaphorin\_4c\_prec\_mus  
992854 semaphorin

[illegible]

2204229740132ext2\_cura\_56  
2204229740132\_cura\_54  
2204229742\_cura\_54  
q64151 semaphorin\_4c\_prec\_mus  
q92854 semaphorin

DRYTHDPVSPRPGSCENNWHRRHGATSSSELPDNEVKKHPWEEQGPRWSRPLVAK  
 DRNTHDPVSPRPGSCANNWHRRHGATSSSELPDNEVKKHPWEEQGPRWSRPLVAK  
 DRNTHDPVSPRPGSCANNWHRRHGATSSSELPDNEVKKHPWEEQGPRWSRPLVAK  
 ARNTHDPVSPRPGSCANNWHRRHGATSSSELPDNEVKKHPWEEQGPRWSRPLVAK  
 VRRNGPWPVBRPGCATDSEARVATVSSSELPDNEVKKHPWEEQGPRWSRPLVAK

204229740132ext2\_cura\_56  
204229740132\_cura\_54  
204229742\_cura\_54  
q64151 semaphorin\_4c\_prec\_mus  
q92854 semaphorin

[illegible]

204229740132ext2\_cura\_56  
204229740132\_cura\_54  
204229742\_cura\_54  
q64151 semaphorin\_4c\_prec\_mus  
q92854 semaphorin

[illegible]

204229740132ext2\_cura\_56  
204229740132\_cura\_54  
204229742\_cura\_54  
q64151\_semaphorin\_4c\_prec\_mus  
q92854\_semaphorin

[illegible]

204229740132ex12\_cura\_56  
204229740132\_cura\_54  
204229742\_cura\_54  
q64151\_semaphorin\_4c\_prec\_mus  
q92854\_semaphorin

YTCILPVPQGWERLCEGKKRKGWACCGQWHTLFQP  
EESV  
GSQDPAEQPGSFLYDTGLQALVMAAQSRHSGPYRCYSEEQGTRLAAESYLVAVVAGSS  
QNGVFAKAESPKYGLMGRKNLLIFNLSEGDGVIQCLSEERVKNKTVQVIAKHVLEVKVV

204229740132ext2\_cura\_56  
204229740132\_cura\_54  
204229742\_cura\_54  
q64151 semaphorin\_4c\_prec\_mus  
q92854 semaphorin

VTLEAPLENGLVWLAVVALGAVCLVLLLVLSLRRRLREELEKGAKASERTLVYPLE  
PKPVVAPTLSSVOTEGSRIATKVLVASTQGSSPPTPAVQATSSGAILTPPKPAPTGTSC

**Fig. 15B**

T020T"0502000T

204229740132ext2_cura_56	~
204229740132_cura_54	~
204229742_cura_54	~
q64151_semaphorin_4c_prec_mus	LPKEPASPFRPGPETDEKLWDPVGYYS DGS LKIVPGHARCQPGGGPPSPPPGIPGQPL
q92854_semaphorin	PKIVINTVPQLHSEKTYLKSSDNRLMSLFLFFVLFCLFFYNCYKGYLPRQCLKFRS
204229740132ext2_cura_56	~
204229740132_cura_54	~
204229742_cura_54	~
q64151_semaphorin_4c_prec_mus	PSPTRLHLGGGRNSNANGYVRLLQGGEDRGSGHPLPELADELRRKLQQRQPLPDSNPEE
q92854_semaphorin	ALLIGKKPKSDFCDREQSLKETLVEPGFSQQNGEHPKPALDTGYETEQDTITTSKVPTD
204229740132ext2_cura_56	~
204229740132_cura_54	~
204229742_cura_54	~
q64151_semaphorin_4c_prec_mus	SSV~
q92854_semaphorin	REDSQRIDDLSARDKPFVDVKCELKFADSDADGD

Fig. 15C



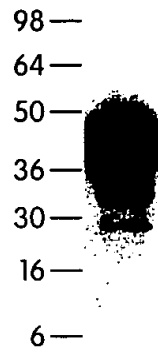


Fig. 16

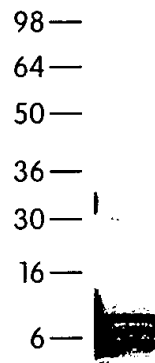


Fig. 17

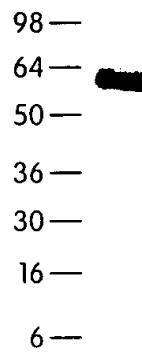


Fig. 18

FOOT " 0502000T

Tissue Source	Relative Expression (%)				
	3445452	17089878	1795045.0.61	20422974	20936375.0.104
Endothelial cells	0.00	0.00	1.88	1.11	8.72
Endothelial cells (treated)	0.00	0.01	4.58	1.99	9.74
Pancreas	2.05	0.32	2.68	5.63	16.49
Pancreatic ca. CAPAN 2	0.01	0.00	0.07	1.91	40.05
Adipose	0.24	1.48	6.70	10.01	51.05
Adrenal gland	0.92	0.43	1.36	9.54	75.26
Thyroid	21.17	0.00	1.96	6.25	30.78
Salivary glands	7.59	0.13	1.56	5.67	24.66
Pituitary gland	0.05	0.07	1.11	10.73	10.81
Brain (fetal)	0.17	15.18	3.59	12.41	25.00
Brain (whole)	1.96	34.15	52.85	28.32	38.16
Brain (amygdala)	1.03	19.89	7.13	7.97	46.33
Brain (cerebellum)	4.64	29.73	76.84	29.32	55.86
Brain (hippocampus)	2.98	28.32	27.17	33.45	57.04
Brain (hypothalamus)	10.51	1.18	12.67	4.12	38.69
Brain (substantia nigra)	6.25	7.18	23.49	16.61	67.36
Brain (thalamus)	4.80	6.00	22.53	13.68	69.26
Spinal cord	1.76	4.24	7.64	29.12	50.70
CNS ca. (glio/astro) U87-MG	0.03	0.00	1.99	2.16	29.73
CNS ca. (glio/astro) U-118-MG	0.00	3.54	1.25	2.34	12.33
CNS ca. (astro) SW1783	0.00	0.17	0.00	0.74	13.03
CNS ca.* (neuro;met) SK-N-AS	0.00	0.43	4.30	10.01	93.95
CNS ca. (astro) SF-539	0.07	0.14	0.00	9.81	14.16
CNS ca. (astro) SNB-75	0.00	0.06	0.23	11.58	8.84
CNS ca. (glio) SNB-19	0.01	0.58	0.11	5.15	33.45
CNS ca. (glio) U251	0.01	0.00	0.01	1.58	8.42
CNS ca. (glio) SF-295	0.00	0.00	0.01	3.77	10.44
Heart	33.92	0.01	1.82	7.64	100.00
Skeletal muscle	100.00	0.00	1.00	3.06	79.00
Bone marrow	1.05	3.72	0.43	1.69	18.17
Thymus	0.30	0.21	4.42	6.12	28.52
Spleen	0.14	0.13	2.59	17.43	24.49
Lymph node	0.28	0.28	1.92	10.51	11.74

Fig. 19

SECX	Clone Number	Tissue Expression	Length (nt)	ORF (nt)	Amine Acid Length	Calculate Molecular Weight of Encoded Protein	Protein Similarity (BLASTP Non-Redundant Composite Database)	Protein Similarity (Human Sequence)	Signal Peptide Cleavage Site (nt)	Cellular Localization
1	3445452	Prostate Gland	932	113-796	227	25734.1	Identities 52/128 (40%); Positives 72/128 (56%) with ACC:P31044 Phosphatidylethanolamine e-Binding Protein (PEBP); 23Kd Morphine Binding Protein (P23K) <i>Rattus norvegicus</i> . 187 amino acid residues.	Identities 44/120 (36%); Positives 66/120 (55%) with ACC:P31044 Phosphatidylethanolamine e-Binding Protein (PEBP) <i>Homo sapiens</i> . 186 Amino Acid residues.	yyyy. Most likely cleavage site between positions 22 and 23: VTG-DE.	Outside - Cert=0.7380. Appears to possess a cleavable N-terminal Signal Sequence.
2	4011999	Not Known	734	66-(?)735	223	24499	Identities 55/76 (72%); Positives 61/76 (80%) with ptnr:SP TREMBL-ACC:Q13670 PMS2-Related Protein HPMSR6 <i>Homo sapiens</i> . 270 amino acid residues.	Identities 48/127 (37%); Positives 69/127 (54%) with ptnr:SP TREMBL-ACC:075631 Uroplakin III <i>Homo sapiens</i> . 287 amino acid residues.	yyyy. Most likely cleavage site between positions 27 and 28: SLS-LD.	Plasma Membrane - Cert.=0.8056. Appears to possess a cleavable N-terminal Signal Sequence.
3	17089878 .0.5	Fetal Brain	2762	264-2630	788	88337	Identities 729/788 (92%); Positives 758/788 (96%) with ACC:P79995 Cadherin-10 Precursor <i>Gallus gallus</i> . 789 amino acid residues. Identities 636/650 (97%); Positives 645/650 (99%) with rat cadherin-10. 653 amino acid residues.	Identities 577/790 (73%); Positives 676/790 (85%) with ACC:P55285 Cadherin-6 Precursor (Kidney-Cadherin) <i>Homo sapiens</i> . 790 amino acid residues.	yyyy. Most likely cleavage site between positions 22 and 23:CSECX-EI.	Plasma Membrane - Cert.=0.4600. Appears to possess a cleavable N-terminal Signal Sequence.
4	17089878 .0.6	Fetal Brain	1820	285-1704	473	529226	Identities 445/473 (94%); Positives 465/473 (98%) with ACC:P7995 789 aa Cadherin-10 Precursor	Identities 346/476 (72%); Positives 415/476 (87%) with ACC:P55285, human Cadherin-6 precursor Precursor (790 aa)		Plasma Membrane - Cert.=0.7000. Apparently lacks cleavable N-terminal Signal Sequences.

Fig. 20A

SEC No.	Clone Number	Tissue Expression	Nucleotide Length	Open Reading Frame (nt)	Amine Acid Length	Calculate Molecular Weight	Protein Similarity (BLASTP Non-Redundant Composite Database)	Protein Similarity (Human Sequence)	Signal Peptide Cleavage Site (nt)	Cellular Localization
5	1795045.0.61	Brain, Thalamus, Pituitary Gland	1508	226-1461	411	46054.5	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:000276 Lymphocyte-Associated Receptor of Death 2 <i>Homo sapiens</i> . 510 amino acid residues.	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:000276 Lymphocyte-Associated Receptor of Death 2 <i>Homo sapiens</i> . 510 amino acid residues.		Cytoplasm - Cert.=0.4500. Appears to possess no cleavable N-terminal Signal Sequence.
6	20422974.0.132	Lymphoid Tissue	2155	166-1938	590	66532.5	Identities 497/582 (85%); Positives 536/582 (92%) with ACC:Q64151 Semaphorin I (M-SEMA) FA Factor in Neural Network Development) <i>Mus musculus</i> . 834 amino acid residues.	Identities 247/506 (48%); Positives 330/506 (65%) with ACC:Q92854 Semaphorin <i>Homo sapiens</i> . 862 Amino Acid residues.	yyyy. Most likely cleavage site between positions 20 and 21: GIG-AE.	Microbody (Peroxisome) - Cert.=7480. Appears to possess a cleavable N-terminal Signal Sequence.
7	20422974.2	Lymphoid Tissue	2284	166-1956	596	66969.8	Identities 498/585 (85%); Positives 540/585 (92%) with ACC:Q64151 Semaphorin I (M-SEMA) FA Factor in Neural Network Development) <i>Mus musculus</i> . 834 amino acid residues.	Identities 265/558 (47%); Positives 353/558 (63%) with ACC:Q92854 Semaphorin <i>Homo sapiens</i> . 862 Amino Acid residues.	yyyy. Most likely cleavage site between positions 20 and 21: GIG-AE.	Microbody (Peroxisome) - Cert.=7480. Appears to possess a cleavable N-terminal Signal Sequence.
8	20936375.0.1	Kidney	1930	148-1758	536	60306.7	Identities 453/531 (85%); Positives 482/531 (90%) with ACC:P07106 Bovine DBI-Related Brain Membrane Protein.	Identities 37/91 (40%); Positives 58/91 (63%) with ACC:O75521 DBI-Related Protein <i>Homo sapiens</i> . 364 Amino acid residues.	nnny. Most likely cleavage site between positions 15 and 16:SWC-CC.	Plasma Membrane - Cert.=0.7000. Appears to possess a cleavable N-terminal Signal Sequence.
9	20936785.0.1	Brain, Fetal Brain	930	123-626	167	18440	Identities 167/167 (100%) with Human Transmembrane Protein HTMPN-46.	Identities 167/167 (100%) with Human Transmembrane Protein HTMPN-46.	nnny. Most likely cleavage site between positions 31 and 32:TPR-LS.	Plasma Membrane - Cert.=64000. Appears to possess an uncleavable N-terminal Signal Sequence. Likely a Type IIIa Membrane Protein

Fig. 20B

SEC No.	Clone Number	Tissue Expression	Nucleotide Length	ORF	Amino Acid Length	Calculated Molecular Weight	Protein Similarity (BLASTP Non-Redundant Composite Database)	Protein Similarity (Human Sequence)	Signal Peptide Cleavage Site (nt)	Cellular Localization
10	1795045.0.77	Brain, Thalamus	1737	296-1690	464	51645.6	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:000276 Lymphocyte-Associated Receptor of Death 2 <i>Homo sapiens</i> . 510 amino acid residues.	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:000276 Lymphocyte-Associated Receptor of Death 2 <i>Homo sapiens</i> . 510 amino acid residues.		Cytoplasm- Cert.=0.4500. Appears to possess no cleavable N-terminal Signal Sequence.
11	20422974.0.132_ex12	Lymphoid Tissue, Aorta, Breast, Colon, Foreskin, Germ Cell, Muscle, Prostate, Spleen, Stomach, and Uterus.	2156	166-2040	624	70478.1	Identities 501/599 (83%); Positives 542/599 (90%) with ACC:Q92854 Semaphorin <i>Homo sapiens</i> . 862 Amino Acid residues.	Identities 501/599 (83%); Positives 542/599 (90%) with ACC:Q92854 Semaphorin <i>Homo sapiens</i> . 862 Amino Acid residues.	yyyy. Most likely cleavage site between positions 20 and 21: GIG-AE.	Microbody (Peroxisome)- Cert.=7480. Appears to possess a cleavable N-terminal Signal Sequence.
12	20936375.0.104	Kidney	1930	7-1611	534	60037.3	Identities 453/531 (85%); Positives 482/531 (90%) with ACC:P07106 Bovine DBI-Related Brain Membrane Protein.	Identities 37/91 (40%); Positives 58/91 (63%) with ACC:O75521 DBI-Related Protein <i>Homo sapiens</i> . 364 amino acid residues.		Plasma Membrane - Cert.=0.7300. Appears not to possess a cleavable N-terminal Signal Sequence.

Fig. 20C